

BLASTP 2.2.19+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Reference for compositional score matrix adjustment: Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

7,873,120 sequences; 2,713,143,868 total letters

Query=

Length=412

Sequences producing significant alignments:		Score (Bits)	E Value
ref NP_034677.1	inhibitor of kappaB kinase gamma isoform 1 [...	823	0.0
gb AAK69186.1 AF326207_2	NFkB essential modulator [Mus muscul...	822	0.0
ref NP_001129539.1	inhibitor of kappaB kinase gamma [Mus mus...	820	0.0
ref NP_848705.1	inhibitor of kappaB kinase gamma isoform 2 [...	790	0.0
emb CAM45962.1	inhibitor of kappaB kinase gamma [Mus musculus]	788	0.0
gb AAM44073.1	inhibitor of kappaB kinase gamma [Homo sapiens]	681	0.0
gb AAD12183.1	leucine zipper protein Fip3p [Homo sapiens]	680	0.0

ALIGNMENTS

>ref|NP_034677.1| inhibitor of kappaB kinase gamma isoform 1 [Mus musculus]
 sp|O88522.1|NEMO_MOUSE RecName: Full=NF-kappa-B essential modulator; Short=NEMO;
 AltName:
 Full=NF-kappa-B essential modifier; AltName: Full=Inhibitor
 of nuclear factor kappa-B kinase subunit gamma; Short=IkB
 kinase subunit gamma; Short=I-kappa-B kinase gamma; Short=IKK-gamma;
 Short=IKKG; AltName: Full=IkB kinase-associated
 protein 1; Short=IKKAP1; Short=mFIP-3
 gb|AAC40153.1| NF-kB essential modulator [Mus musculus]
 Length=412

Score = 823 bits (2127), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 412/412 (100%), Positives = 412/412 (100%), Gaps = 0/412 (0%)

Query	1	MNKHPWKNQLSETVQPSGGPAEDQDMLGEESLGGKPAHLHPSEQGTTPETLQRCLEENQE	60
		MNKHPWKNQLSETVQPSGGPAEDQDMLGEESLGGKPAHLHPSEQGTTPETLQRCLEENQE	
Sbjct	1	MNKHPWKNQLSETVQPSGGPAEDQDMLGEESLGGKPAHLHPSEQGTTPETLQRCLEENQE	60
Query	61	LRDAIRQSNQMLRERCEELLHFQVSQREEKEFLMCKFQEARLVERLSLEKLDLRSQREQ	120
		LRDAIRQSNQMLRERCEELLHFQVSQREEKEFLMCKFQEARLVERLSLEKLDLRSQREQ	
Sbjct	61	LRDAIRQSNQMLRERCEELLHFQVSQREEKEFLMCKFQEARLVERLSLEKLDLRSQREQ	120
Query	121	ALKELEQLKKCCQQMAEDKASVKAQVTSLLGELQESQSRLEAATKDRQALEGRIRAVSEQ	180
		ALKELEQLKKCCQQMAEDKASVKAQVTSLLGELQESQSRLEAATKDRQALEGRIRAVSEQ	
Sbjct	121	ALKELEQLKKCCQQMAEDKASVKAQVTSLLGELQESQSRLEAATKDRQALEGRIRAVSEQ	180
Query	181	VRQLESEREVLQQQHSVQVDQLRMQNQSVEAALRMERQAASEEKRKLAQLQAAYHQLFQD	240
		VRQLESEREVLQQQHSVQVDQLRMQNQSVEAALRMERQAASEEKRKLAQLQAAYHQLFQD	
Sbjct	181	VRQLESEREVLQQQHSVQVDQLRMQNQSVEAALRMERQAASEEKRKLAQLQAAYHQLFQD	240
Query	241	YDSHIKSSKGMQLEDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADI	300
		YDSHIKSSKGMQLEDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADI	
Sbjct	241	YDSHIKSSKGMQLEDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADI	300
Query	301	YKADFQAERHAREKLVEKKEYLQEQLQREFNKLKVGCHESARIEDMRKRHVETPQPP	360
		YKADFQAERHAREKLVEKKEYLQEQLQREFNKLKVGCHESARIEDMRKRHVETPQPP	
Sbjct	301	YKADFQAERHAREKLVEKKEYLQEQLQREFNKLKVGCHESARIEDMRKRHVETPQPP	360
Query	361	LLPAPAHHSFHLALSNQRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMIECIE	412
		LLPAPAHHSFHLALSNQRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMIECIE	
Sbjct	361	LLPAPAHHSFHLALSNQRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMIECIE	412

>gb|AAK69186.1|AF326207_2 NFkB essential modulator [Mus musculus]
 gb|AAP47160.1|AF513109_1 kappaB kinase gamma inhibitor [Mus musculus]
 dbj|BAE32372.1| unnamed protein product [Mus musculus]
 emb|CAM45971.1| inhibitor of kappaB kinase gamma [Mus musculus]
 gb|EDL29810.1| inhibitor of kappaB kinase gamma, isoform CRA_b [Mus musculus]
 Length=412

Score = 822 bits (2122), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 411/412 (99%), Positives = 411/412 (99%), Gaps = 0/412 (0%)

Query	1	MNKHPWKNQLSETVQPSGGPAEDQDMLGEESLGGKPAHLHPSEQGTTPETLQRCLEENQE	60
		MNKHPWKNQLSE VQPSGGPAEDQDMLGEESLGGKPAHLHPSEQGTTPETLQRCLEENQE	
Sbjct	1	MNKHPWKNQLSEMVQPSGGPAEDQDMLGEESLGGKPAHLHPSEQGTTPETLQRCLEENQE	60
Query	61	LRDAIRQSNQMLRERCEELLHFQVSQREEKEFLMCKFQEARLVERLSLEKLDLRSQREQ	120
		LRDAIRQSNQMLRERCEELLHFQVSQREEKEFLMCKFQEARLVERLSLEKLDLRSQREQ	
Sbjct	61	LRDAIRQSNQMLRERCEELLHFQVSQREEKEFLMCKFQEARLVERLSLEKLDLRSQREQ	120
Query	121	ALKELEQLKKCCQQMAEDKASVKAQVTSLLGELQESQSRLEAATKDRQALEGRIRAVSEQ	180
		ALKELEQLKKCCQQMAEDKASVKAQVTSLLGELQESQSRLEAATKDRQALEGRIRAVSEQ	
Sbjct	121	ALKELEQLKKCCQQMAEDKASVKAQVTSLLGELQESQSRLEAATKDRQALEGRIRAVSEQ	180

NEMO alignemts
Mus musculus versus *Homo sapiens*

Query	181	VRQLESEREVLQQQHSVQVDQLRMQNQSVEAALRMERQAASEEKRKLAQLQAAYHQLFQD	240
		VRQLESEREVLQQQHSVQVDQLRMQNQSVEAALRMERQAASEEKRKLAQLQAAYHQLFQD	
Sbjct	181	VRQLESEREVLQQQHSVQVDQLRMQNQSVEAALRMERQAASEEKRKLAQLQAAYHQLFQD	240
Query	241	YDSHIKSSKGMQLEDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADI	300
		YDSHIKSSKGMQLEDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADI	
Sbjct	241	YDSHIKSSKGMQLEDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADI	300
Query	301	YKADFQAERHAREKLVEKKEYLQEQLQREFNKLKVGCHESARIEDMRKRHVETPQPP	360
		YKADFQAERHAREKLVEKKEYLQEQLQREFNKLKVGCHESARIEDMRKRHVETPQPP	
Sbjct	301	YKADFQAERHAREKLVEKKEYLQEQLQREFNKLKVGCHESARIEDMRKRHVETPQPP	360
Query	361	LLPAPAHHSFHLALSNNRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMECIE	412
		LLPAPAHHSFHLALSNNRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMECIE	
Sbjct	361	LLPAPAHHSFHLALSNNRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMECIE	412

>ref|NP_001129539.1| inhibitor of kappaB kinase gamma [Mus musculus]
 gb|AAM54725.1| inhibitor of kappaB kinase gamma [Mus musculus]
 emb|CAM45963.1| inhibitor of kappaB kinase gamma [Mus musculus]
 Length=430

Score = 820 bits (2117), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 411/412 (99%), Positives = 411/412 (99%), Gaps = 0/412 (0%)

Query	1	MNKHPWKNQLSETVQPSGGPAEDQDMLGEESSLGKPAMLHLPSEQGTPETLQRCLEENQE	60
		MNKHPWKNQLSE VQPSGGPAEDQDMLGEESSLGKPAMLHLPSEQGTPETLQRCLEENQE	
Sbjct	19	MNKHPWKNQLSEMVQPSGGPAEDQDMLGEESSLGKPAMLHLPSEQGTPETLQRCLEENQE	78
Query	61	LRDAIRQSNQMLRERCEELLHFQVSQREEKEFLMCKFQEARKLVERLSLEKLDLRSQREQ	120
		LRDAIRQSNQMLRERCEELLHFQVSQREEKEFLMCKFQEARKLVERLSLEKLDLRSQREQ	
Sbjct	79	LRDAIRQSNQMLRERCEELLHFQVSQREEKEFLMCKFQEARKLVERLSLEKLDLRSQREQ	138
Query	121	ALKELEQLKKCQQQMAEDKASVKAQVTSLLGELQESQSRLEAATKDRQALEGRIRAVSEQ	180
		ALKELEQLKKCQQQMAEDKASVKAQVTSLLGELQESQSRLEAATKDRQALEGRIRAVSEQ	
Sbjct	139	ALKELEQLKKCQQQMAEDKASVKAQVTSLLGELQESQSRLEAATKDRQALEGRIRAVSEQ	198
Query	181	VRQLESEREVLQQQHSVQVDQLRMQNQSVEAALRMERQAASEEKRKLAQLQAAYHQLFQD	240
		VRQLESEREVLQQQHSVQVDQLRMQNQSVEAALRMERQAASEEKRKLAQLQAAYHQLFQD	
Sbjct	199	VRQLESEREVLQQQHSVQVDQLRMQNQSVEAALRMERQAASEEKRKLAQLQAAYHQLFQD	258
Query	241	YDSHIKSSKGMQLEDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADI	300
		YDSHIKSSKGMQLEDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADI	
Sbjct	259	YDSHIKSSKGMQLEDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADI	318
Query	301	YKADFQAERHAREKLVEKKEYLQEQLQREFNKLKVGCHESARIEDMRKRHVETPQPP	360
		YKADFQAERHAREKLVEKKEYLQEQLQREFNKLKVGCHESARIEDMRKRHVETPQPP	
Sbjct	319	YKADFQAERHAREKLVEKKEYLQEQLQREFNKLKVGCHESARIEDMRKRHVETPQPP	378
Query	361	LLPAPAHHSFHLALSNNRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMECIE	412
		LLPAPAHHSFHLALSNNRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMECIE	
Sbjct	379	LLPAPAHHSFHLALSNNRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMECIE	430

>ref|NP_848705.1| inhibitor of kappaB kinase gamma isoform 2 [Mus musculus]
 gb|AAH21431.1| Ikbkg protein [Mus musculus]
 dbj|BAC29672.1| unnamed protein product [Mus musculus]
 emb|CAM45972.1| inhibitor of kappaB kinase gamma [Mus musculus]
 gb|EDL29809.1| inhibitor of kappaB kinase gamma, isoform CRA_a [Mus musculus]
 Length=411

Score = 790 bits (2040), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 410/412 (99%), Positives = 410/412 (99%), Gaps = 1/412 (0%)

Query	1	MNKHPWKNQLSETVQPSGGPAEDQDMLGEESSLGKPAMLHLPSEQGTPETLQRCLEENQE	60
		MNKHPWKNQLSE VQPSGGPAEDQDMLGEESSLGKPAMLHLPSEQGTPETLQRCLEENQE	
Sbjct	1	MNKHPWKNQLSEMVQPSGGPAEDQDMLGEESSLGKPAMLHLPSEQGTPETLQRCLEENQE	60

Query	61	LRDAIRQSNQMLRERCEELLHFQVSQREEKEFLMCKFQEARLVERLSLEKLDLRSQREQ	120
Sbjct	61	LRDAIRQSNQMLRERCEELLHFQVSQREEKEFLMCKFQEARLVERLSLEKLDLRSQREQ	120
Query	121	ALKELEQLKKCQQMAEDKASVKAQVTSLLGELQESQSRLEAATKDRQALEGRIRAVSEQ	180
Sbjct	121	ALKELEQLKKCQQ MAEDKASVKAQVTSLLGELQESQSRLEAATKDRQALEGRIRAVSEQ	179
Query	181	VRQLESEREVLQQQHSVQVDQLRMQNQSVEAALRMRQAASEEKRKLAQLQAAYHQLFQD	240
Sbjct	180	VRQLESEREVLQQQHSVQVDQLRMQNQSVEAALRMRQAASEEKRKLAQLQAAYHQLFQD	239
Query	241	YDSHIKSSKGMQLEDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADI	300
Sbjct	240	YDSHIKSSKGMQLEDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADI	299
Query	301	YKADFQAERHAREKLVEKKEYLQEQLEQLQREFNKLKVGCHESARIEDMRKRHVETPQPP	360
Sbjct	300	YKADFQAERHAREKLVEKKEYLQEQLEQLQREFNKLKVGCHESARIEDMRKRHVETPQPP	359
Query	361	LLPAPAHHSFHLALSNQRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMECIE	412
Sbjct	360	LLPAPAHHSFHLALSNQRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMECIE	411

>emb|CAM45962.1| inhibitor of kappaB kinase gamma [Mus musculus]
 Length=429

Score = 788 bits (2035), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 410/412 (99%), Positives = 410/412 (99%), Gaps = 1/412 (0%)

Query	1	MNKHWPKNQLSETVQPSGGPAEDQDMLGEESLGGKPAHLHPSEQGTPTLQRCLEENQE	60
Sbjct	19	MNKHWPKNQLSEMVQPSGGPAEDQDMLGEESLGGKPAHLHPSEQGTPTLQRCLEENQE	78
Query	61	LRDAIRQSNQMLRERCEELLHFQVSQREEKEFLMCKFQEARLVERLSLEKLDLRSQREQ	120
Sbjct	79	LRDAIRQSNQMLRERCEELLHFQVSQREEKEFLMCKFQEARLVERLSLEKLDLRSQREQ	138
Query	121	ALKELEQLKKCQQMAEDKASVKAQVTSLLGELQESQSRLEAATKDRQALEGRIRAVSEQ	180
Sbjct	139	ALKELEQLKKCQQ MAEDKASVKAQVTSLLGELQESQSRLEAATKDRQALEGRIRAVSEQ	197
Query	181	VRQLESEREVLQQQHSVQVDQLRMQNQSVEAALRMRQAASEEKRKLAQLQAAYHQLFQD	240
Sbjct	198	VRQLESEREVLQQQHSVQVDQLRMQNQSVEAALRMRQAASEEKRKLAQLQAAYHQLFQD	257
Query	241	YDSHIKSSKGMQLEDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADI	300
Sbjct	258	YDSHIKSSKGMQLEDLRQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPVLKAQADI	317
Query	301	YKADFQAERHAREKLVEKKEYLQEQLEQLQREFNKLKVGCHESARIEDMRKRHVETPQPP	360
Sbjct	318	YKADFQAERHAREKLVEKKEYLQEQLEQLQREFNKLKVGCHESARIEDMRKRHVETPQPP	377
Query	361	LLPAPAHHSFHLALSNQRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMECIE	412
Sbjct	378	LLPAPAHHSFHLALSNQRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMECIE	429

>ref|NP_003630.1| inhibitor of kappa light polypeptide gene enhancer in B-cells,
 kinase gamma [Homo sapiens]
 ref|NP_001093326.1| inhibitor of kappa light polypeptide gene enhancer in B-cells,
 kinase gamma [Homo sapiens]
 ref|NP_001093327.1| inhibitor of kappa light polypeptide gene enhancer in B-cells,

kinase gamma [Homo sapiens]
 sp|Q9Y6K9.2|NEMO_HUMAN RecName: Full=NF-kappa-B essential modulator; Short=NEMO;
 AltName:
 Full=NF-kappa-B essential modifier; AltName: Full=Inhibitor
 of nuclear factor kappa-B kinase subunit gamma; Short=Ikb
 kinase subunit gamma; Short=I-kappa-B kinase gamma; Short=IKK-gamma;
 Short=IKKG; AltName: Full=Ikb kinase-associated
 protein 1; Short=IKKAP1; AltName: Full=FIP-3
 gb|AAD38081.1|AF091453_1 NEMO protein [Homo sapiens]
 gb|AAF99679.1|AF261086_1 NF-kB essential modulator NEMO [Homo sapiens]
 gb|AAL27012.1|AF277315_2 NFkappaB essential modulator [Homo sapiens]
 gb|AAC36330.1|Ikb kinase gamma subunit [Homo sapiens]
 emb|CAB93146.1|NF-KB Essential Modulator [Homo sapiens]
 gb|AAH00299.1|IKBKG protein [Homo sapiens]
 gb|AAH12114.1|IKBKG protein [Homo sapiens]
 gb|AAH50612.1|IKBKG protein [Homo sapiens]
 gb|AAV38427.1|inhibitor of kappa light polypeptide gene enhancer in B-cells,
 kinase gamma [Homo sapiens]
 gb|AAX41620.1|inhibitor of kappa light polypeptide gene enhancer in B-cells
 kinase gamma [synthetic construct]
 gb|AAH46922.1|IKBKG protein [Homo sapiens]
 gb|ABM82309.1|inhibitor of kappa light polypeptide gene enhancer in B-cells,
 kinase gamma [synthetic construct]
 gb|ABM85486.1|inhibitor of kappa light polypeptide gene enhancer in B-cells,
 kinase gamma [synthetic construct]
 dbj|BAG10959.1|NF-kappa-B essential modulator [synthetic construct]
 Length=419

Score = 683 bits (1763), Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 362/419 (86%), Positives = 381/419 (90%), Gaps = 7/419 (1%)

Query	1	MNKHWPKNQLSETVQPSGGPAEDQDMLGEESSLGKPAMHLHPSEQGTPETLQRCLEENQE	60
		MN+H WK+QL E VQPSGGPA DQD+LGEES LGKPAMHLHPSEQG PETLQRCLEENQE	
Sbjct	1	MNRHLWKSQLCMVQPSGGPAADQDVLGEESPLGKPAMHLHPSEQGAPETLQRCLEENQE	60
Query	61	LRDAIRQSNQMLRERCEELLHFQVSQREEKEFLMCKFQEARKLVERLSLEKLDLRSQREQ	120
		LRDAIRQSNQ+LRERCEELLHFQ SQREEKEFLMCKFQEARKLVERL LEKLDL+ Q+EQ	
Sbjct	61	LRDAIRQSNQILRERCEELLHFQASQREEKEFLMCKFQEARKLVERLGLEKLDLKRQKEQ	120
Query	121	ALKELEQLKKCQQQMAEDKASVKAQVTSLLGELQESQSRLEAATKDRQALEGRIRAVSEQ	180
		AL+E+E LK+CQQQMAEDKASVKAQVTSLLGELQESQSRLEAATK+ QALEGR RA SEQ	
Sbjct	121	ALREVEHLKRCQQQMAEDKASVKAQVTSLLGELQESQSRLEAATKECQALEGRARAASEQ	180
Query	181	VRQLESEREVLQQQHSVQVDQLRMQNSVEAALRMERQAASEEKRKLAQLQAAYHQLFQD	240
		RQLESERE LQQQHSVQVDQLRMQ QSVEAALRMERQAASEEKRKLAQLQ AYHQLFQ+	
Sbjct	181	ARQLESEREALQQQHSVQVDQLRMQGSVEAALRMERQAASEEKRKLAQLQVAYHQLFQE	240
Query	241	YDSHIKSS-----KGMQLEDLRLQQLQQAEEALVAKQELIDKLKEEAEQHKIVMETVPV	293
		YD+HIKSS +GMQLEDL+QQLQQAEEALVAKQE+IDKLKEEAEQHKIVMETVPV	
Sbjct	241	YDNHIKSSVVGSEKRGKGMQLEDLKLQQLQQAEEALVAKQEVIDKLKEEAEQHKIVMETVPV	300
Query	294	LKAQADIYKADFQAERHAREKLVEKKEYLQEQLQREFNKLKVGCHESARIEDMRKRH	353
		LKAQADIYKADFQAER AREKL EKKE LQEQLQLORE++KLK C ESARIEDMRKRH	
Sbjct	301	LKAQADIYKADFQAERQAREKLAEKKELLQEQLQLOREYSKLGKASCQESARIEDMRKRH	360
Query	354	VETPQPPLLPAPAHHSFHLALSQRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMCIE	412
		VE Q PL PAPA+ S LAL +QRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMCIE	
Sbjct	361	VEVSQAPLPPAPAYLSSPLALPSQRRSPPEEPPDFCCPKCQYQAPDMDTLQIHVMCIE	419